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DATA NOTE

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Draft genome sequence of *Staphylococcus* sp. EZ-P03 isolated from a mesophilic anaerobic digester

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Abstract

Objectives: *Staphylococcus* species of the family *Staphylococcaceae* are facultatively anaerobic Gram-positive cocci growing in clusters, pairs and occasionally in short chains. Staphylococci can be detected in different environments. They are common commensals, but some can also cause infections in humans. Hence, their investigation is required to understand ecology and genetics and to create an opportunity for comparative studies.

Data description: In this study, we report the determination of a draft genome sequence of *Staphylococcus* sp. strain EZ-P03 which was isolated from anaerobically digested chicken waste materials. The draft genome of *Staphylococcus* sp. EZ-P03 constituted a total of 62 contigs (> 500 bp) amounting to 2,689,358 bp with a G+C content of 37.3% and a N50 contig size of 126,562 bp. The whole genome shotgun project of *Staphylococcus* sp. strain EZ-P03 has been deposited at DDBJ/ENA/GenBank under the accession number QPMO00000000.

Keywords: Draft genome, *Firmicutes*, *Staphylococcus* sp., Chicken manure, Laboratory-scale mesophilic reactor

Objective

Staphylococcus species of the family *Staphylococcaceae* are facultatively anaerobic Gram-positive cocci growing in clusters, pairs and occasionally in short chains. Staphylococci grow by respiration or fermentation and can be found in different environmental niches. *S. aureus* and *S. epidermidis* species are common commensals but have a high pathogenic potential. *S. saprophyticus*, *S. haemolyticus*, *S. simulans*, *S. cohnii*, *S. warneri* and others can also cause infections in human [1, 2]. Some *Staphylococcus* species with proteolytic activities have been shown to survive in various anaerobic digesters [3, 4]. The anaerobic digestion process is an appropriate technology for different agricultural wastes utilization [5, 6]; however, it is also important to develop effective hygiene and sanitation procedures to minimize the potential disease transfer risk [7, 8]. Genome analysis of species belonging to the genus *Staphylococcus* is required to understand their ecology and genetics and to create an opportunity for comparative studies.

Data description

Staphylococcus sp. EZ-P03 was isolated from a mesophilic anaerobic digester operated at high ammonia levels (> 6.0 NH_4–N g L^{-1}) and fed with chicken manure as monosubstrate [4]. The strain *Staphylococcus* sp. EZ-P03 was cultured at + 37 °C on Luria agar for 48 h under microaerophilic conditions. Genomic DNA from the bacterial cells (washed with sterile phosphate buffer solution) was extracted with the FastDNA spin kit (#116540600; MP Biomedicals). DNA quantification and quality control were performed by agarose gel electrophoresis and measurement with a NanoDrop 2000 spectrophotometer (#ND-2000; Thermo Fisher Scientific) confirming an optical density 260/280 of between 1.8 and 2 and finally stored at − 20 °C. The bacterial strain EZ-P03 was initially identified based on morphological,

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